In the specification:

Please amend paragraph [0054] of the published application to correspond to the paragraph starting at page 9, line 24 through to page 10, line 7, which was submitted as indicated below in the originally filed application, as follows:

In another embodiment, agents that interact with (e.g. bind to) a CDCP1 polypeptide are identified in a cell-free assay system where a sample expressing a CDCP1 polypeptide is contacted with a candidate agent and the ability of the candidate agent to interact with the polypeptide is determined. Preferably, the ability of a candidate agent to interact with a. CDCP1 polypeptide is compared to a reference range or control. In a preferred embodiment, a first and second sample comprising native or recombinant CDCP1 polypeptide are contacted with a candidate agent or a control agent and the ability of the candidate agent to interact with the polypeptide is determined by comparing the difference in interaction between the candidate agent and control agent. If desired, this assay may be used to screen a plurality (e.g. a library) of candidate agents using a plurality of CDCP1 polypeptide samples. Preferably, the polypeptide is first immobilized, by, for example, contacting the polypeptide with an immobilized antibody which specifically recognizes and binds it, or by contacting a purified preparation of polypeptide with a surface designed to bind proteins. The polypeptide may be partially or completely purified (e.g. partially or completely free of other polypeptides) or part of a cell lysate. Further, the polypeptide may be a fusion protein comprising the CDCP1 polypeptide or a biologically active portion thereof and a domain such as glutathionine-S-transferase. Alternatively, the polypeptide can be biotinylated using techniques well known to those of skill in the art (e.g. biotinylation kit, Pierce Chemicals; Rockford, Ill.). The ability of the candidate agent to interact with the polypeptide can be duplicated by methods <u>known</u> ~~kiown~~ to those of skill in the art.

Please amend paragraph [0057] of the published application to correspond to the paragraph starting at page 10, line 28 through to page 11, line 12, which was submitted as indicated below in the originally filed application, as follows:

In yet another embodiment, agents that competitively interact with (i.e. competitively

binding to) a CDCP1 polypeptide are identified in a competitive binding assay and the ability of the candidate agent to interact with the CDCP1 polypeptide is determined. Preferably, the ability of a candidate agent to interact with a CDCP1 polypeptide is compared to a reference range or control. In a preferred embodiment, a first and second population of cells expressing both a CDCP1 polypeptide and a protein which is known to interact with the CDCP1 polypeptide are contacted with a candidate agent or a control agent. The ability of the candidate agent to competitively interact with the CDCP1 polypeptide is then determined by comparing the interaction in the first and second population of cells. In another embodiment, an alternative second population or a further population of cells may be contacted with an agent which is known to competitively interact with a CDCP1 polypeptide. Alternatively, agents that competitively interact with a CDCP1 polypeptide are identified in a cell-free assay system by contacting a first and second sample comprising a CDCP1 polypeptide and a protein known to interact with the CDCP1 polypeptide with a candidate agent or a control agent. The ability of the candidate agent to competitively interact with the CDCP1 polypeptide is then determined by comparing the interaction in the first and second sample. In another embodiment, an alternative second sample or a further sample comprising a CDCP1 polypeptide may be contacted with an agent which is known to competitively interact with a CDCP1 polypeptide. In any case, the CDCP1 polypeptide and known interacting protein may be expressed naturally or may be recombinantly expressed; the candidate agent may be added exogenously, or be expressed naturally or recombinantly.

Please amend the paragraph starting at page 15, line 30 through to page 16, line 4 as follows:

Pharmaceutical compositions of the present invention suitable for oral administration may be presented as discrete units such as capsules, cachets or tablets, each containing a predetermined amount of the active agent, as a powder or granules, or as a solution or a suspension in an aqueous liquid, a non-aqueous liquid, an oil-in-water emulsion or a water-in-oil liquid emulsion. Such compositions may be prepared by any of the methods of pharmacy but all methods include the step of bringing into association the active agent with the carrier, which constitutes one or more necessary ingredients. In general, the compositions are prepared by uniformly and intimately mixing ~~admixing~~ the active agent with liquid carriers or finely divided

solid carriers or both, and then, if necessary, shaping the product into the desired presentation. For example, a tablet may be prepared by compression or moulding, optionally with one or more accessory ingredients.

Please amend paragraph [0093] of the published application to correspond to the paragraph at page 18, lines 14-16, which was submitted as indicated below in the originally filed application, as follows:

Pharmaceutical compositions adapted for vaginal administration may be presented as pessaries, tampons, creams, gels, pastes, foams or spray compositions. These may comprise emollients ~~emofliients~~ or bases as commonly used in the art.

Please amend the paragraph at page 19, lines 1-11 as follows:

CDCP1 polypeptides may also be of use in the treatment and/or prophylaxis of ovarian cancer. Accordingly, provided is a method for the treatment and/or prophylaxis of ovarian cancer comprising administering a therapeutically effective amount of a composition comprising a CDCP1 polypeptide, preferably as a vaccine. Also provided is the use of a CDCP1 polypeptide for the manufacture of a medicament for the treatment and/or prophylaxis of ovarian cancer. Where they are provided for use with the methods of the invention CDCP1 polypeptides are preferably provided in isolated form. More preferably the CDCP1 polypeptides have been purified to at least some extent. CDCP1 polypeptides can also be produced using recombinant methods, synthetically produced or produced by a combination of these methods. CDCP1 polypeptides may be provided in substantially pure form, that is to say free, to a substantial extent, from other proteins.

Please amend the paragraph at page 27, lines 21-27 as follows:

Direct injection of naked DNA or through the use of microparticle bombardment (e.g. GENE GUN ~~Gene Gun~~®; Biolistic, Dupont) or by coating it with lipids can also be used in gene therapy. Cell-surface receptors/transfecting compounds or through encapsulation in liposomes,

microparticles or microcapsules or by administering the nucleic acid in linkage to a peptide which is known to enter the nucleus or by administering it in linkage to a ligand predisposed to receptor-mediated endocytosis (See Wu & Wu, 1987, J. Biol. Chem., 262:4429-4432) can be used to target cell types which specifically express the receptors of interest.

Please amend the paragraph at page 30, lines 3-17 as follows:

Methods to obtain full length cDNAs or to extend short cDNAs are well known in the art, for example RACE (Rapid amplification of cDNA ends; e.g. Frohman et al., 1988, Proc. Natl. Acad. Sci USA 85:8998-9002). Recent modifications of the technique, exemplified by the MARATHON ~~Marathon~~ ™ technology (Clontech Laboratories Inc.) have significantly simplified the search for longer cDNAs. This technology uses cDNAs prepared from mRNA extracted from a chosen tissue followed by the ligation of an adaptor sequence onto each end. PCR is then carried out to amplify the missing 5'-end of the cDNA using a combination of gene specific and adaptor specific oligonucleotide primers. The PCR reaction is then repeated using nested primers which have been designed to anneal with the amplified product, typically an adaptor specific primer that anneals further 3' in the adaptor sequence and a gene specific primer that anneals further 5' in the known gene sequence. The products of this reaction can then be analysed by DNA sequencing and a full length cDNA constructed either by joining the product directly to the existing cDNA to give a complete sequence, or carrying out a separate full length PCR using the new sequence information for the design of the 5' primer.

Please amend the paragraph at page 30, lines 19-36 as follows:

A further aspect of the invention relates to a vaccine composition of use in the treatment and/or prophylaxis of ovarian cancer. A CDCP1 polypeptide or nucleic acid as described above can be used in the production of vaccines for treatment and/or prophylaxis of ovarian cancer. Such material can be antigenic and/or immunogenic. Antigenic includes a protein or nucleic acid that is capable of being used to raise antibodies or indeed is capable of inducing an antibody response in a subject. Immunogenic material includes a protein or nucleic acid that is capable of eliciting an immune response in a subject. Thus, in the latter case, the protein or nucleic acid may

be capable of not only generating an antibody response but, in addition, a non-antibody based immune responses, i.e. a cellular or humoral response. It is well known in the art that it is possible to identify those regions of an antigenic or immunogenic polypeptide that are responsible for the antigenicity or immunogenicity of said polypeptide, i.e. an epitope or epitopes. Amino acid and peptide characteristics well known to the skilled person can be used to predict the antigenic index (a measure of the probability that a region is antigenic) of a CDCP1 polypeptide. For example, but without limitation, the `Peptidestructure` program (Jameson and Wolf, 1988, CABIOS, 4(1):181) and a technique referred to as `Threading` (Altuvia Y. et al., 1995, J. Mol. Biol. 249:244) can be used. Thus, the CDCP1 polypeptides may include one or more such epitopes or be sufficiently similar to such regions so as to retain their antigenic/immunogenic properties.

Please amend the paragraph at page 33, lines 7-13 as follows:

After electrophoresis the gel plates were pried ~~prised~~ open, the gel placed in a tray of fixer (10% acetic acid, 40% ethanol, 50% water) and shaken overnight. The gel was then primed for 30 minutes by shaking in a primer solution (7.5% acetic acid, 0.05% SDS in Milli-Q water) followed by incubation with a fluorescent dye (0.06% OGS dye in 7.5% acetic acid) with shaking for 3hrs. A preferred fluorescent dye is disclosed in U.S. Pat. No. 6,335,446. SYPRO® ~~Sypro~~ Red (Molecular Probes, Inc., Eugene, Oreg.) is a suitable alternative dye for this purpose.

Please amend the paragraph at page 33, lines 14-16 as follows:

A digital image of the stained gel was obtained by scanning on a STORM® ~~Storm~~ Scanner (Molecular Dynamics Inc, USA) in the blue fluorescence mode. The captured image was used to determine the area of the gel to excise for in-gel proteolysis.

Please amend the paragraph starting at page 33, line 18 through to page 34, line 8 as follows:

Each vertical lane of the gel was excised using a stainless steel scalpel blade. Proteins were processed using in-gel digestion with trypsin (Modified trypsin, Promega, Wis., USA) to

generate tryptic digest peptides. Recovered samples were divided into two. Prior to MALDI analysis samples were desalted and concentrated using C18 ZIP TIPS ~~Zip Tips~~ ™(Millipore, Bedford, Mass.). Samples for tandem mass spectrometry were purified using a nano LC system (LC Packings, Amsterdam, The Netherlands) incorporating C18 SPE material. Recovered peptide pools were analysed by MALDI-TOF-mass spectrometry (Voyager STR, Applied Biosystems, Framingham, Mass.) using a 337 nm wavelength laser for desorption and the reflectron mode of analysis. Pools were also analyzed by nano-LC tandem mass spectrometry (LC/MS/MS) using a Micromass Quadrupole Time-of-Flight (Q-TOF) mass spectrometer (Micromass, Altrincham, UK). For partial amino acid sequencing and identification of cancer cell membrane proteins, uninterpreted tandem mass spectra of tryptic peptides were searched against a database of public domain proteins constructed of protein entries in the non-redundant database held by the National Centre for Biotechnology Information (NCBI) which is accessible at http://www.ncbi.nlm.nih.gov/ using the SEQUEST search program (Eng et al., 1994, J. Am. Soc. Mass Spectrom. 5:976-989), version v.C.1. Criteria for database identification included: the cleavage specificity of trypsin; the detection of a suite of a, b and y ions in peptides returned from the database, and a mass increment for all Cys residues to account for carbamidomethylation. Following identification of proteins through spectral-spectral correlation using the SEQUEST program, masses detected in MALDI-TOF mass spectra were assigned to tryptic digest peptides within the proteins identified. In cases where no amino acid sequences could be identified through searching with uninterpreted MS/MS spectra of tryptic digest peptides using the SEQUEST program, tandem mass spectra of the peptides were interpreted manually, using methods known in the art. (In the case of interpretation of low-energy fragmentation mass spectra of peptide ions see Gaskell et al., 1992, Rapid Commun. Mass Spectrom. 6:658-662). The method described in WO 02/21139 was also used to interpret mass spectra.

Please amend the paragraph at page 34, lines 20-28 as follows:

Reactions containing 5 ng cDNA, SYBR® green sequence detection reagents (PE Biosystems) and sense and antisense primers were assayed on an ABI7700 sequence detection system (PE Biosystems). The PCR conditions were 1 cycle at 50°C for 2 min, 1 cycle at 95°C for

10 min, and 40 cycles of 95°C for 15s, 65°C for 1 min. The accumulation of PCR product was measured in real time as the increase in SYBR® green fluorescence, and the data were analysed using the Sequence Detector program v1.6.3 (PE Biosystems). Standard curves relating initial template copy number to fluorescence and amplification cycle were generated using the amplified PCR product as a template, and were used to calculate CDCP1 copy number in each sample.